

SEQUENCE LISTING

<110> Alexander H. Borchers
Donna T. Ward
Susan M. Freier

<120> ANTISENSE MODULATION OF ABC TRANSPORTER MHC 1 EXPRESSION

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10024369-121701

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gga gct tct ctc gca tgg ctg ggg aca gta ctg cta ctt ctc gcc gac	96
Gly Ala Ser Leu Ala Trp Leu Gly Thr Val Leu Leu Leu Leu Ala Asp	
20 25 30	
tgg gtg ctg ctc cgg acc gcg ctg ccc cgc ata ttc tcc ctg ctg gtg	144
Trp Val Leu Leu Arg Thr Ala Leu Pro Arg Ile Phe Ser Leu Leu Val	
35 40 45	
ccc acc gcg ctg cca ctg ctc cgg gtc tgg gcg gtg ggc ctg agc cgc	192
Pro Thr Ala Leu Pro Leu Leu Arg Val Trp Ala Val Gly Leu Ser Arg	
50 55 60	
tgg gcc gtg ctc tgg ctg ggg gcc tgc ggg gtc ctc agg gca acg gtt	240
Trp Ala Val Leu Trp Leu Gly Ala Cys Gly Val Leu Arg Ala Thr Val	
65 70 75 80	
ggc tcc aag agc gaa aac gca ggt gcc cag ggc tgg ctg gct gct ttg	288
Gly Ser Lys Ser Glu Asn Ala Gly Ala Gln Gly Trp Leu Ala Ala Leu	
85 90 95	
aag cca tta gct gcg gca ctg ggc ttg gcc ctg ccg gga ctt gcc ttg	336
Lys Pro Leu Ala Ala Ala Leu Gly Leu Ala Leu Pro Gly Leu Ala Leu	
100 105 110	
ttc cga gag ctg atc tca tgg gga gcc ccc ggg tcc gcg gat agc acc	384
Phe Arg Glu Leu Ile Ser Trp Gly Ala Pro Gly Ser Ala Asp Ser Thr	
115 120 125	
agg cta ctg cac tgg gga agt cac cct acc gcc ttc gtt gtc agt tat	432
Arg Leu Leu His Trp Gly Ser His Pro Thr Ala Phe Val Val Ser Tyr	
130 135 140	
gca gcg gca ctg ccc gca gca gcc ctg tgg cac aaa ctc ggg agc ctc	480
Ala Ala Ala Leu Pro Ala Ala Ala Leu Trp His Lys Leu Gly Ser Leu	
145 150 155 160	
tgg gtg ccc ggc ggt cag ggc ggc tct gga aac cct gtg cgt cgg ctt	528
Trp Val Pro Gly Gly Gln Gly Gly Ser Gly Asn Pro Val Arg Arg Leu	
165 170 175	
cta ggc tgc ctg ggc tcg gag acg cgc cgc ctc tcg ctg ttc ctg gtc	576

10024369-12701

Leu Gly Cys	Leu Gly Ser Glu Thr Arg Arg	Leu Ser Leu Phe Leu Val	
180	185	190	
ctg gtg gtc ctc tcc tct ctt ggg gag atg gcc att cca ttc ttt acg			624
Leu Val Val Leu Ser Ser Leu Gly Glu Met Ala Ile Pro Phe Phe Thr			
195	200	205	
ggc cgc ctc act gac tgg att cta caa gat ggc tca gcc gat acc ttc			672
Gly Arg Leu Thr Asp Trp Ile Leu Gln Asp Gly Ser Ala Asp Thr Phe			
210	215	220	
act cga aac tta act ctc atg tcc att ctc acc ata gcc agt gca gtg			720
Thr Arg Asn Leu Thr Leu Met Ser Ile Leu Thr Ile Ala Ser Ala Val			
225	230	235	240
ctg gag ttc gtg ggt gac ggg atc tat aac aac acc atg ggc cac gtg			768
Leu Glu Phe Val Gly Asp Gly Ile Tyr Asn Asn Thr Met Gly His Val			
245	250	255	
cac agc cac ttg cag gga gag gtg ttt ggg gct gtc ctg cgc cag gag			816
His Ser His Leu Gln Gly Glu Val Phe Gly Ala Val Leu Arg Gln Glu			
260	265	270	
acg gag ttt ttc caa cag aac cag aca ggt aac atc atg tct cgg gta			864
Thr Glu Phe Phe Gln Gln Asn Gln Thr Gly Asn Ile Met Ser Arg Val			
275	280	285	
aca gag gac acg tcc acc ctg agt gat tct ctg agt gag aat ctg agc			912
Thr Glu Asp Thr Ser Thr Leu Ser Asp Ser Leu Ser Glu Asn Leu Ser			
290	295	300	
tta ttt ctg tgg tac ctg gtg cga ggc cta tgt ctc ttg ggg atc atg			960
Leu Phe Leu Trp Tyr Leu Val Arg Gly Leu Cys Leu Leu Gly Ile Met			
305	310	315	320
ctc tgg gga tca gtg tcc ctc acc atg gtc acc ctg atc acc ctg cct			1008
Leu Trp Gly Ser Val Ser Leu Thr Met Val Thr Leu Ile Thr Leu Pro			
325	330	335	
ctg ctt ttc ctt ctg ccc aag aag gtg gga aaa tgg tac cag ttg ctg			1056
Leu Leu Phe Leu Leu Pro Lys Lys Val Gly Lys Trp Tyr Gln Leu Leu			
340	345	350	
gaa gtg cag gtg cgg gaa tct ctg gca aag tcc agc cag gtg gcc att			1104
Glu Val Gln Val Arg Glu Ser Leu Ala Lys Ser Ser Gln Val Ala Ile			
355	360	365	
gag gct ctg tcg gcc atg cct aca gtt cga agc ttt gcc aac gag gag			1152
Glu Ala Leu Ser Ala Met Pro Thr Val Arg Ser Phe Ala Asn Glu Glu			
370	375	380	
ggc gaa gcc cag aag ttt agg gaa aag ctg caa gaa ata aag aca ctc			1200
Gly Glu Ala Gln Lys Phe Arg Glu Lys Leu Gln Glu Ile Lys Thr Leu			
385	390	395	400
aac cag aag gag gct gtg gcc tat gca gtc aac tcc tgg acc act agt			1248
Asn Gln Lys Glu Ala Val Ala Tyr Ala Val Asn Ser Trp Thr Thr Ser			
405	410	415	

10024369 12101

att .tca ggt atg ctg ctg aaa gtg gga atc ctc tac att ggt ggg cag 1296
 Ile Ser Gly Met Leu Leu Lys Val Gly Ile Leu Tyr Ile Gly Gly Gln
 420 425 430
 ctg gtg acc agt ggg gct gta agc agt ggg aac ctt gtc aca ttt gtt 1344
 Leu Val Thr Ser Gly Ala Val Ser Ser Gly Asn Leu Val Thr Phe Val
 435 440 445
 ctc tac cag atg cag ttc acc cag gct gtg gag gta ctg ctc tcc atc 1392
 Leu Tyr Gln Met Gln Phe Thr Gln Ala Val Glu Val Leu Leu Ser Ile
 450 455 460
 tac ccc aga gta cag aag gct gtg ggc tcc tca gag aaa ata ttt gag 1440
 Tyr Pro Arg Val Gln Lys Ala Val Gly Ser Ser Glu Lys Ile Phe Glu
 465 470 475 480
 tac ctg gac cgc acc cct cgc tgc cca ccc agt ggt ctg ttg act ccc 1488
 Tyr Leu Asp Arg Thr Pro Arg Cys Pro Pro Ser Gly Leu Leu Thr Pro
 485 490 495
 tta cac ttg gag ggc ctt gtc cag ttc caa gat gtc tcc ttt gcc tac 1536
 Leu His Leu Glu Gly Leu Val Gln Phe Gln Asp Val Ser Phe Ala Tyr
 500 505 510
 cca aac cgc cca gat gtc tta gtg cta cag ggg ctg aca ttc acc cta 1584
 Pro Asn Arg Pro Asp Val Leu Val Leu Gln Gly Leu Thr Phe Thr Leu
 515 520 525
 cgc cct ggc gag gtg acg gcg ctg gtg gga ccc aat ggg tct ggg aag 1632
 Arg Pro Gly Glu Val Thr Ala Leu Val Gly Pro Asn Gly Ser Gly Lys
 530 535 540
 agc aca gtg gct gcc ctg ctg cag aat ctg tac cag ccc acc ggg gga 1680
 Ser Thr Val Ala Ala Leu Leu Gln Asn Leu Tyr Gln Pro Thr Gly Gly
 545 550 555 560
 cag ctg ctg ttg gat ggg aag ccc ctt ccc caa tat gag cac cgc tac 1728
 Gln Leu Leu Leu Asp Gly Lys Pro Leu Pro Gln Tyr Glu His Arg Tyr
 565 570 575
 ctg cac agg cag gtg gct gca gtg gga caa gag cca cag gta ttt gga 1776
 Leu His Arg Gln Val Ala Ala Val Gly Gln Glu Pro Gln Val Phe Gly
 580 585 590
 aga agt ctt caa gaa aat att gcc tat ggc ctg acc cag aag cca act 1824
 Arg Ser Leu Gln Glu Asn Ile Ala Tyr Gly Leu Thr Gln Lys Pro Thr
 595 600 605
 atg gag gaa atc aca gct gct gca gta aag tct ggg gcc cat agt ttc 1872
 Met Glu Glu Ile Thr Ala Ala Ala Val Lys Ser Gly Ala His Ser Phe
 610 615 620
 atc tct gga ctc cct cag ggc tat gac aca gag gta gac gag gct ggg 1920
 Ile Ser Gly Leu Pro Gln Gly Tyr Asp Thr Glu Val Asp Glu Ala Gly
 625 630 635 640
 agc cag ctg tca ggg ggt cag cga cag gca gtg gcg ttg gcc cga gca 1968
 Ser Gln Leu Ser Gly Gly Gln Arg Gln Ala Val Ala Leu Ala Arg Ala

10024369-12701
 10024369-12701

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Leu Ile Arg Lys Pro Cys Val Leu Ile Leu Asp Asp Ala Thr Ser Ala				
	660	665	670	
ctg gat gca aac agc cag tta cag gtg gag cag ctc ctg tac gaa agc				2064
Leu Asp Ala Asn Ser Gln Leu Gln Val Glu Gln Leu Leu Tyr Glu Ser				
	675	680	685	
cct gag cgg tac tcc cgc tca gtg ctt ctc atc acc cag cac ctc agc				2112
Pro Glu Arg Tyr Ser Arg Ser Val Leu Leu Ile Thr Gln His Leu Ser				
	690	695	700	
ctg gtg gag cag gct gac cac atc ctc ttt ctg gaa gga ggc gct atc				2160
Leu Val Glu Gln Ala Asp His Ile Leu Phe Leu Glu Gly Gly Ala Ile				
705	710	715	720	
cgg gag ggg gga acc cac cag cag ctc atg gag aaa aag ggg tgc tac				2208
Arg Glu Gly Gly Thr His Gln Gln Leu Met Glu Lys Lys Gly Cys Tyr				
	725	730	735	
tgg gcc atg gtg cag gct cct gca gat gct cca gaa tga				2247
Trp Ala Met Val Gln Ala Pro Ala Asp Ala Pro Glu				
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PATENT

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TOTAL 69E4201

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